We claim:

1. A method of determining the stage of disease caused by HCMV infection, comprising the step of:

    determining expression levels in a first human cell sample of one or more genes which are induced or repressed by HCMV, wherein the first human cell sample comprises cells of a patient infected with HCMV, wherein the first human cell sample consists essentially of HCMV-infected cells, wherein the expression levels of the one or more genes correlates with stage of disease progression of the HCMV infection.

2. A method of determining the extent of tissue damage caused by HCMV infection, comprising the step of:

    determining expression levels in a first human cell sample of one or more genes which are induced or repressed by HCMV, wherein the first human cell sample comprises cells of a patient infected with HCMV, wherein the first human cell sample consists essentially of HCMV-infected cells, wherein the expression levels of the one or more genes correlates with extent of tissue damage caused by the HCMV infection.

3. A method for screening to identify candidate drugs for preventing disease symptoms caused by HCMV, comprising the steps of:

    contacting human cells with HCMV and a test agent;

    determining expression levels of one or more genes which are induced or repressed by HCMV;

    identifying a test agent as a candidate drug if the test agent causes the human cells to express the one or more genes at a level at which the human cells express the one or more genes in the absence of HCMV.

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4.   The method of claim 1, 2, or 3 wherein the one or more genes are selected from the group consisting of those genes identified in Table 1 as induced or repressed by HCMV.

5.   The method of claim 1, 2, or 3 wherein the one or more genes are induced or repressed to a level which is at least two-fold different than the level of expression in the absence of HCMV.

6.   The method of claim 1, 2, or 3 wherein the one or more genes are induced or repressed to a level which is at least four-fold different than the level of expression in the absence of HCMV.

7.   The method of claim 1, 2, or 3 wherein the one or more genes are induced or repressed to a level which is at least eight-fold different than the level of expression in the absence of HCMV.

8.   The method of claim 1, 2, or 3 wherein the one or more genes are induced or repressed to a level which is at least ten-fold different than the level of expression in the absence of HCMV.

9.   The method of claim 1, 2, or 3 wherein the one or more genes are induced or repressed to a level which is at least fifteen-fold different than the level of expression in the absence of HCMV.

10. The method of claim 1, 2, or 3 in which the step of determining is performed by measuring amounts of mRNA expressed by the one or more genes.

11. The method of claim 1, 2, or 3 in which the step of determining is performed by measuring amounts of protein expressed by the one or more genes..

12. The method of claim 1, 2, or 3 in which the step of determining is performed using an array of oligonucleotides.

13. The method of claim 1, 2, or 3 in which the step of determining us performed using serial analysis of gene expression.

14. The method of claim 1, 2, or 3 in which the step of determining is performed using hybridization of nucleic acids on a solid support.

15. The method of claim 1, 2, or 3 in which the step of determining is performed using cDNA which is made using mRNA collected from the human cells as a template.

16. The method of claim 1, 2, or 3 in which a fluorescent label is used to determine expression levels.

17. The method of claim 1, 2, or 3 in which the one or more genes comprise *HLA-E*.

18. The method of claim 1, 2, or 3 in which the one or more genes comprise *Ro/SSA*.

19. The method of claim 1, 2, or 3 in which the one or more genes comprise *lipocortin-1*.

20. The method of claim 1, 2, or 3 in which the one or more genes comprise *cPLA2*.

21. The method of claim 1, 2, or 3 in which the one or more genes comprise *COX-2*.

22. The method of claim 1, 2, or 3 in which the one or more genes comprise *thrombospondin-1*.

23. The method of claim 1, 2, or 3 in which the one or more genes comprise *MITF*.

24. The method of claim 1, 2, or 3 in which expression levels of at least 2 genes are determined.

25. The method of claim 1, 2, or 3 in which expression levels of at least 5 genes are determined.

26. The method of claim 1, 2, or 3 in which expression levels of at least 10 genes are determined.

27. The method of claim 1, 2, or 3 in which expression levels of at least 15 genes are determined.

28. The method of claim 1, 2, or 3 in which expression levels of at least 20 genes are determined.

29. The method of claim 1, 2, or 3 in which expression levels of at least 25 genes are determined.

30. The method of claim 1, 2, or 3 in which expression levels of at least 30 genes are determined.

31. The method of claim 1, 2, or 3 in which expression levels of at least 50 genes are determined.

32. The method of claim 1, 2, or 3 in which expression levels of at least 100 genes are determined.

33. The method of claim 1, 2, or 3 in which expression levels of at least 200 genes are determined.

34. The method of claim 1, 2, or 3 in which expression levels of at least 250 genes are determined.

35. The method of claim 1, 2, or 3 in which expression levels of at least 500 genes are determined.

36. The method of claim 1, 2, or 3 in which expression levels of at least 1000 genes are determined.

37. The method of claim 1, 2, or 3 in which the human cells are fibroblasts.

38. The method of claim 1, 2, or 3 in which the human cells are lymphocytes.

39. The method of claim 1, 2, or 3 in which the human cells are epithelial cells.

40. The method of claim 1, 2, or 3 in which the human cells are lung epithelial cells.

41. The method of claim 1, 2, or 3 in which the human cells are neuronal cells.

42. The method of claim 1 or 2 further comprising the step of:

determining expression levels in a second human cell sample of said one or more genes which are induced or repressed by HCMV, wherein the second human cell sample comprises cells of said patient, wherein the second human cell sample consists essentially of uninfected cells, wherein the first and the second human cell sample comprise the same cell type;

comparing the expression levels determined in the first and the second human cell samples.

43. The method of claim 1 or 2 wherein the expression levels determined in the first human cell sample are compared to expression levels determined for a reference sample of uninfected human cells of the same cell type.

44. The method of claim 1 further comprising the step of:

correlating the expression levels of the one or more genes with the stage of disease progression of the HCMV infection.

45. The method of claim 2 further comprising the step of:

correlating the expression levels of the one or more genes with the extent of tissue damage caused by the HCMV infection.

46. A method for identifying a subset of genes which are improved targets for drug development, comprising the steps of:

(a) comparing expression levels of at least two genes in two cell samples, wherein the two cell samples are the same but for differences caused by a selected environmental, genetic, disease, or developmental agent;

(b) identifying a set of genes whose expression levels differ between the two cell samples;

(c) searching a database to identify an unselected environmental agent, gene, disease, or developmental stage previously associated with expression or altered expression of individual members of the set of genes;

(d) identifying a common biological feature between the selected environmental, genetic, disease, or developmental difference of step (a) and the unselected environmental agent, gene, disease, or developmental stage identified in step (c), wherein identification of a common biological feature between two environmental, genetic, disease, or developmental phenomena which both affect expression of a common gene identifies the common gene

as being a member of a subset of genes which are improved targets for drug development.

47. A computer-readable medium having computer-executable instructions for performing steps comprising:

    (a) comparing expression levels of at least two genes in two cell samples, wherein the two cell samples are the same but for differences caused by a selected environmental, genetic, disease, or developmental agent;

    (b) identifying a set of genes whose expression levels differ between the two cell samples;

    (c) searching a database to identify an unselected environmental agent, gene, disease, or developmental stage previously associated with expression or altered expression of individual members of the set of genes;

    (d) identifying a common biological feature between the selected environmental, genetic, disease, or developmental difference of step (a) and the unselected environmental agent, gene, disease, or developmental stage identified in step (c), wherein identification of a common biological feature between two environmental, genetic, disease, or developmental phenomena which both affect expression of a common gene identifies the common gene as being a member of a subset of genes which are improved targets for drug development.